<u>IN THE SPECIFICATION</u>:

Please amend the second paragraph on page 13 of the specification as follows:

Next, the process proceeds to Step 202 in FIG. 2 and constructs a fixed-length partial sequence table 103. When constructing the fixed-length partial sequence table 103, partial sequences 102 having a length of s at the head and tail ~~end among~~ ends of all the input sequences 101 is entered into the table 103 as shown in FIG. 4. If the length s of the partial sequence is taken longer, the probability of occurrence of coincidence between the lengths s can be decreased regardless of the presence of a true overlap between the input sequences, so that the processing time can be shorten. However, if the length s of the partial sequence is excessively taken too long, the sensitivity for searching for an overlap will become lower. In the present invention, the value s has a lower limit which is represented by an expression (1) described below, in order to shorten the processing time.

Please amend last paragraph on page 15 of the specification as follows:

Suppose that an exact matching 501 with a certain input sequence 502 is found when referring to the fixed-length partial sequence table 103. Only the occurrence of the exact matching 501 having a length of s is not sufficient as a condition for adding this sequence 502 to the cluster because this exact matching may occur merely by coincidence. Therefore, it should be verified that both of the entire overlapping portions 503 are sufficiently similar to each other and the assembling is possible without contradiction between them by comparing one sequence with the other (Step 205 in FIG. 2). In this sequence comparison, a position of the exact matching whose length is s between the consensus sequence and the input sequence is apparent, so that a high [[peed]] <u>speed</u> algorithm described in Zhang, Z. et al., J. Comput. Biol., 7 (1-2): 203-14, 2000 is used.

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